WHAT IS CLAIMED IS:

1. An isolated polynucleotide from corynebacteria which contains a polynucleotide sequence selected from the group consisting of:

a) a polynucleotide which is at least 70% identical to a polynucleotide encoding a polypeptide containing the amino acid sequence of SEQ ID NO: 2,

b) a polynucleotide encoding a polypeptide containing an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2,

c) a polynucleotide which is complementary to the polynucleotides of a) or b), and

d) a polynucleotide containing at least 15 consecutive bases of the polynucleotide sequence of a), b) or c).

2. The polynucleotide according to Claim 1 which is a DNA replicatable in corynebacteria.

3. The polynucleotide according to Claim 2 that is a recombinant DNA.

4. The polynucleotide according to Claim 1 which is an RNA.

5. The polynucleotide according to Claim 2 containing the nucleic acid sequence as shown in SEQ ID NO:1.

6. Replicatable DNA according to Claim 2 containing:

(i) the nucleotide sequence shown in SEQ ID NO:1, or

(ii) at least one sequence corresponding to sequence (i) within the degeneracy of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii), and optionally

(iv) neutral sense mutations in (i).

7. The polynucleotide according to Claim 2 encoding a polypeptide containing the amino acid sequence as shown in SEQ ID NO:2.

8. A fermentation process for the preparation of an L-amino acid, comprising the following steps:

a) fermentation of the L-lysine-producing corynebacteria in which at least the gpm gene or nucleotide sequences coding therefor are amplified and, in particular, overexpressed,

b) enrichment of the L-amino acid in the medium or in the cells of the bacteria, and

c) isolation of the L-amino acid.

9. The process according to Claim 8 wherein the L-amino acid is L-lysine.

10. The process according to Claim 8, characterized in that bacteria are used in which other genes of the biosynthetic pathway of the desired L-amino acid are additionally amplified.

11. The process according to Claim 8, characterized in that bacteria are used in which the metabolic pathways which reduce the formation of L-lysine are at least partially switched off.

12. The process according to Claim 8, characterized in that a strain transformed with a plasmid vector is used and the plasmid vector carries the nucleotide sequence coding for the gpm gene.

13. The process according to one of Claims 7 to 10, characterized in that corynebacteria which produce L-lysine are used.

14. The process according to Claim 10, characterized in that the dapA gene coding for dihydrodipicolinate synthase is simultaneously overexpressed.

15. The process according to Claim 10, characterized in that a DNA fragment which confers S-(2-aminoethyl)cysteine resistance is simultaneously amplified.

16. The process according to Claim 10, characterized in that the gap gene coding for glyceraldehyde 3-phosphate dehydrogenase is simultaneously overexpressed.

17. The process according to Claim 10, characterized in that the tpi gene coding for triose phosphate isomerase is simultaneously overexpressed.

18. The process according to Claim 10, characterized in that the pgk gene coding for 3-phosphoglycerate kinase is simultaneously overexpressed.

19. The process according to Claim 10, characterized in that the pyc gene coding for pyruvate carboxylase is simultaneously overexpressed.

20. A process for the production of DNA of genes which develop an action corresponding to the opcA gene comprising employment of the polynucleotide sequences according to Claim 1 as primers in a polymerase chain reaction.

21. A hybridization probe comprising a polynucleotide sequence according to claim 1.

22. Coryneform microorganisms transformed by the introduction of the replicatable DNA according to one of Claims 1 or 6.

23. Microorganisms according to claim 22 from the genus Corynebacterium.